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SNiPlay: A Web-Based Tool For Detection, Management And Analysis Of SNP.

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The rapidly increasing amount of re-sequencing and genotyping data generated by large-scale genetic diversity projects requires the development of integrated bioinformatics tools able to efficiently manage, analyze, and combine genetic data with the genome's structure and with external data available.
In this context, we developed SNiPlay, a flexible, user-friendly and integrative web-based tool dedicated to polymorphism discovery and analysis. It integrates:
1) a pipeline, freely accessible through the internet, combining existing software with new tools to detect SNPs and to compute different kinds of statistical indices and graphical layouts for SNP data. From Sanger sequencing traces, multiple sequence alignments or genotyping data given as input, SNiPlay detects SNPs and insertion/deletion events. In a second time, it sends sequences and genotyping data into a series of modules in charge of various post-processes: physical mapping to a reference genome, annotation (genomic position, intron/exon location, synonymous/non-synonymous substitutions), SNP frequency determination in user-defined groups, haplotype reconstruction and networking, linkage disequilibrium evaluation, and diversity analysis (Pi, Watterson's Theta, Tajima's D).
2) a database storing polymorphisms, genotyping data and sequences of grapevine produced by nationally-funded public projects. It allows one to retrieve SNPs using various filters (such as genomic position, missing data, polymorphism type, allele frequency), to compare SNP patterns between populations, and to export genotyping data or sequences in various formats.

SNiPlay is available at: http://www.sniplay.cirad.fr/.

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